

**Claim 12**, lines 1 and 2, change "one of claims 1 to 5" to read -- claim 1 -- ;

**Please amend claim 24 as follows:**

*A18 SW C24-7*  
-- **Claim 24**. (amended) Method according to claim 13, characterized in that the SAT is a cytoplasmic SAT of plant origin or an SAT of bacterial origin, and that the SAT is a plant SAT or a native SAT of bacterial origin [as defined in one of claims 3 to 5 or 9 to 11]. --

**Claim 25**, lines 1 and 2, change "either of claims 23 and 24" to read -- claim 23 -- ;

**Claim 27**, lines 1 and 2, change "either of claims 25 and 26" to read -- claim 25 -- ;

**Claim 29**, lines 1 and 2, change "either of claims 27 and 28" to read -- claim 27 -- ;

**Please amend claim 32 as follows:**

*A2*  
-- **Claim 32**. (amended) Fusion protein according to claim 31, characterized in that the SAT is a cytoplasmic SAT of plant origin or an SAT of bacterial origin, and that the SAT is a plant SAT or a native SAT of bacterial origin [as defined in claims 24 to 30]. --

**Claim 33**, lines 2 and 3, change "either of claims 31 and 32" to read -- claim 31 -- ;

Please ~~amend~~ claim 40 as follows:

A3  
-- Claim 40. (amended) Chimeric gene according to [one of claims 34 to 39] claim 34, characterized in that the nucleic acid sequence which encodes an SAT encodes an SAT in that the SAT which is overexpressed in plant cells is a cysteine-sensitive SAT [as defined in claims 2 to 30]. --

Please ~~amend~~ claim 41 as follows:

A4  
-- Claim 41. (amended) Chimeric gene according to [one of claims 34 to 39] claim 34, characterized in that the nucleic acid sequence which encodes an SAT is the nucleic acid sequence encoding a transit peptide/SAT fusion protein and that the SAT is heterologous with the transit peptide [according to claim 33]. --

Claim ~~42~~, line 4, change "one of claims 34 to 41" to read -- claim 34 -- ;

Please ~~amend~~ claim 43 as follows:

A5  
-- Claim 43. (amended) Method of transforming host organisms, characterized in that at least one nucleic acid sequence according to claim 33, or a chimeric gene comprising a coding sequence as well as heterologous 5' and 3' regulatory sequences, which are able to function in a host organism, and that the coding sequence comprises at least one nucleic acid sequence which encodes an SAT [according to one of claims 34 to 41], is integrated into the genome of the said host organism. --

Please amend claim 44 as follows:

A6  
-- Claim 44. (amended) Method according to claim 43, by means of the vector [according to claim 42] for transforming a host organism, characterized in that it contains at least one chimeric gene comprising a coding sequence as well as heterologous 5' and 3' regulatory sequences, which are able to function in a host organism, and that the coding sequence comprises at least one nucleic acid sequence which encodes an SAT [according to claim 42]. --

Claim 45, lines 1 and 2, change "either of claims 43 and 44" to read -- claim 43 -- ;

Please amend claim 49 as follows:

A7  
-- Claim 49. (amended) Transformed host organism, characterized in that it comprises at least one nucleic acid sequence according to claim 33, or a chimeric gene comprising a coding sequence as well as heterologous 5' and 3' regulatory sequences, which are able to function in a host organism, and that the coding sequence comprises at least one nucleic acid sequence which encodes an SAT [according to one of claims 34 to 41]. --

Please amend claim 50 as follows:

A8  
Cm't  
-- Claim 50. (amended) Host organism according to claim 49, characterized in that it is obtained by the method of transforming host organisms, characterized in that at least one

*A8  
concl.*

nucleic acid sequence encoding a transit peptide/SAT fusion protein, characterized in that the SAT is heterologous with the transit peptide, or a chimeric gene comprising a coding sequence as well as heterologous 5' and 3' regulatory sequences, which are able to function in a host organism, and that the coding sequence comprises at least one nucleic acid sequence which encodes an SAT, is integrated into the genome of the said host organism [according to one of claims 43 to 48]. --

**Please amend claim 51 as follows:**

*A9*

-- **Claim 51.** (amended) Plant cell, characterized in that it comprises at least one nucleic acid sequence according to claim 33, or a chimeric gene comprising a coding sequence as well as heterologous 5' and 3' regulatory sequences, which are able to function in a host organism, characterized in that the coding sequence comprises at least one nucleic acid sequence which encodes an SAT [according to one of claims 34 to 41]. --

**Please amend claim 53 as follows:**

*A10*

-- **Claim 53.** (amended) Plant according to claim 52, characterized in that the plant is regenerated from a plant cell, and that it comprises at least one nucleic acid sequence encoding a transit peptide/SAT fusion protein, characterized in that the SAT is heterologous with the transit peptide [according to claim 51]. --